AMENDMENTS TO THE SPECIFICATION:

Please replace paragraphs 1 and 2 on page 18 with the following paragraphs:

For detection of the M39-GUS minigenome and the subgenomic RNA derived from the M39-GUS minigenome, we used the GUS oligonucleotide (SEQ ID NO.: 2) (5'-GACCCACACTTTGCCGTAATGAGTGACCGCA-3') that hybridizes specifically with the gus gene present in the minigenome and with its messenger RNA, or the GUS 297 oligonucleotide (SEQ ID NO.: 3) (5'-GACCCACACTTTGCCGTAATGAG-3').

Amplification of the DNA was accomplished by PCR using as the matrix 10 µL of the RT reactions. For amplication of the genomic RNA, we used oligonucleotide 1.7, which hybridizes in positions 1,660 and 1,676 of the genomic RNA, or oligonucleotide 1.8, which hybridizes in positions 1,849 and 1,870. For amplification of the subgenomic RNAs, we used each of the antisense oligonucleotides described above together with an oligonucleotide having the leader sequence of TGEV (Leader oligonucleotide, (SEQ ID NO.: 4) (5'-AGATTTTGTCTTCGGACACCAACTCG-3'). The M39-GUS minigenome was detected using the antisense GUS or GUS 297 nucleotide together with oligonucleotide 19949, which hybridizes between positions 3,228 and 3,245 in the minigenome.

Please replace Table 1 on page 18 with the following:

Table 1

Oligonucleotides used in the RT-PCR reactions for detection of the sgmRNAs of TGEV			
ORF	Oligonucleotide (-)	Oligonucleotide (+)	Expected size
1	CTTGATGCACTAACTTCTG (SEQ ID NO.:5) (Oligonucleotide 336)	CAGGATCCTGTAGACAAGTGTGTG (SEQ ID NO.:6) (Oligonucleotide 1.7)	1200
		GGCATGCTTGCTACTAGCTTGGTTGGTGC (SEQ ID NO.: 7) (Oligonucleotide 1.8)	1100
S	TAACCTGCACTCACTACCCC (SEQ ID NO. 8)	Leader	374
3a/ 3b[a]	TCAGCATGAGCTAACCACG (SEQ ID NO.:9)	Leader	615/935
M	GGCTATTATGGCCCGTTGTTTTGG (SEQ ID NO.:10)	Leader	667/960
N	TAGATTGAGAGCGTGACCTTG (SEQ ID NO.:11)	Leader	537/1335
E[b]	GCGCATGCAATCACACGC (SEQ ID NO.:12)	Leader	76/369/ 1062
7	TCTGGTTTCTGCTAAACTCC (SEQ ID NO.:13)	Leader	191/1341
a) the oligonucleotide used hybridizes in gene 3b for detection of both sgmRNA ea/eb and for detection of sgmRNA 3b.			
b) the oligonucleotide used hybridizes in the 5'-terminal of the M gene in order to amplify sgmRNA E, including part of the M ORF.			

Please replace Table 2 on page 21 with the following:

Table 2

Oligonucleotides used for amplification and cloning of regions A and B			
Region	Oligonucleotide (-)	Oligonucleotide (+)	Zone of the amplified genome (nt)
A1	GGGTCGACGAAATATTTGTCTTTCTAT GAAATC (SEQ ID NO.:14)	CCGTCGACATGGCACCTCTGACAGTGCGAGC (SEQ ID NO.:15)	100-649
A2	GGGTCGACCGTTCTTGAGGACTTTGA CCTTAAAATTG (SEQ ID NO. 16)	CCGTCGACCATCACCAGGCTTAATATCACCC (SEQ ID NO.: 17)	599-1149
A3	GGGTCGACTTTCTGGCAAAGTTAAGG GTGTC (SEQ ID NO.:18)	CCGTCGACACGATTGTCTGGAACCACAAATGT TGGC (SEQ ID NO.:19)	1099-1649
A4	GGGTCGACGCTTTTACGATTGTAAACT ACAAGCC (SEQ ID NO.:20)	CCGTCGACTTCAAATGATGAACCAAGTTTTGC (SEQ ID NO.:21)	1599-2144
B	GGGTCGACCAAATACCAACTGGCACA CAAGATCC (SEQ ID NO.:22)	CCGTCGACAATTCTTCAGTGCAAGCACCTACT GTC (SEQ ID NO.: 23)	12195-12763

Please replace paragraph 2 on page 22 with the following paragraph:

The RNA from the infected cells was purified in passage 3, and the minigenomes and subgenomic mRNAs of the minigenomes were detected by RT-PCR. To detect the minigenome and the subgenomic mRNAs, we used an RT reaction using the GUS 297 oligonucleotide (SEQ ID NO.: 24) (5'-GACCACACTTTGCCGTAATGAG-3'). The minigenome was amplified by PCR using the GUS 297 and 19949 oligonucleotides (SEQ ID NO.: 25) (5'-CTTGGTGGATCTGTTGCC-3'). The subgenomic mRNA was amplified by PCR using the GUS 297 and leader oligonucleotides. The products of the RT-PCRs were analyzed by agarose gel electrophoresis together with markers for molecule size.

Please replace paragraph 3 on page 24 with the following paragraph:

To locate the position of the ES, zone A was subdivided into four fragments of 550 nt, which overlapped for a distance of 50 nt (Figure 9B). These fragments, in addition to region B, were amplified by PCR, and each fragment was cloned in the M39-GUS minigenome directly under the control of the optimizied TRS, following the conserved sequence 5'-CUAAAC-3' and the sequence that flanks the 3'-side of the CS [sic; GUS] sequence (SEQ ID NO.:26) (5'ACGTCGACGA-3') (Figure 10).

Please insert the paper copy of the SEQUENCE LISTING submitted herewith between the last page of the specification on page 37 and the first page of the claims on page 38.